SEQUENCE LISTING

<110> Lowe, Keith S.
Gordon-Kamm, William J.
Klein, Theodore M.
Rasco-Gaunt, Sonriza
Cahoon, Rebecca E.
Sun, Xifan
Hoester, George J.
Gregory, Carolyn A.
Nadimpalli, Ramgopal

<120> Transcriptional Activator Nucleic Acids, Polypeptides, and Methods of Use Thereof

<130> 0943

<140> 09/435,054
<141> 1999-11-08

<150> 60/107,643
<151> 1998-11-09

<160> 23

<170> FastSEQ for Windows Version 3.0

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<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (69)...(902)

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Met Asp Ser Ser Ser Phe Leu Pro Ala Ala Gly Ala Glu Asn
1 5 10

ggc tcg gcg gcg ggc ggc gcc aac aat ggc ggc gct gct cag cag cat 158
Gly Ser Ala Ala Gly Gly Ala Asn Asn Gly Gly Ala Ala Gln Gln His
15 20 25 30

gcg gcg ccg gcg atc cgc gag cag gac cgg ctg atg ccg atc gcg aac 206
Ala Ala Pro Ala Ile Arg Glu Gln Asp Arg Leu Met Pro Ile Ala Asn
35 40 45

gtg atc cgc atc atg cgg cgc gtg ctg ccg gcg cac gcc aag atc tcg 254
Val Ile Arg Ile Met Arg Arg Val Leu Pro Ala His Ala Lys Ile Ser
50 55 60

gac gac gcc aag gag acg atc cag gag tgc gtg tcg gag tac atc agc 302
Asp Asp Ala Lys Glu Thr Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser
65 70 75

ttc atc acg ggg gag gcc aac gag cgg tgc cag cgg gag cag cgc aag 350
Phe Ile Thr Gly Glu Ala Asn Glu Arg Cys Gln Arg Glu Gln Arg Lys

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      80                  85                  90

acc atc acc gcc gag gac gtg ctg tgg gcc atg agc cgc ctc ggc ttc      398
Thr Ile Thr Ala Glu Asp Val Leu Trp Ala Met Ser Arg Leu Gly Phe
 95                 100                 105                 110

gac gac tac gtc gag ccg ctc ggc gcc tac ctc cac cgc tac cgc gag      446
Asp Asp Tyr Val Glu Pro Leu Gly Ala Tyr Leu His Arg Tyr Arg Glu
                115                 120                 125

ttc gag ggc gac gcg cgc ggc gtc ggg ctc gtc ccg ggg gcc gcc cca      494
Phe Glu Gly Asp Ala Arg Gly Val Gly Leu Val Pro Gly Ala Ala Pro
            130                 135                 140

tcg cgc ggc ggc gac cac cac ccg cac tcc atg tcg cca gcg gcg atg      542
Ser Arg Gly Gly Asp His His Pro His Ser Met Ser Pro Ala Ala Met
        145                 150                 155

ctc aag tcc cgc ggg cca gtc tcc gga gcc gcc atg cta ccg cac cac      590
Leu Lys Ser Arg Gly Pro Val Ser Gly Ala Ala Met Leu Pro His His
    160                 165                 170

cac cac cac cac gac atg cag atg cac gcc gcc atg tac ggg gga acg      638
His His His His Asp Met Gln Met His Ala Ala Met Tyr Gly Gly Thr
175                 180                 185                 190

gcc gtg ccc ccg ccg gcc ggg cct cct cac cac ggc ggg ttc ctc atg      686
Ala Val Pro Pro Pro Ala Gly Pro Pro His His Gly Gly Phe Leu Met
                195                 200                 205

cca cac cca cag ggt agt agc cac tac ctg cct tac gcg tac gag ccc      734
Pro His Pro Gln Gly Ser Ser His Tyr Leu Pro Tyr Ala Tyr Glu Pro
            210                 215                 220

acg tac ggc ggt gag cac gcc atg gct gca tac tat gga ggc gcc gcg      782
Thr Tyr Gly Gly Glu His Ala Met Ala Ala Tyr Tyr Gly Gly Ala Ala
        225                 230                 235

tac gcg ccc ggc aac ggc ggg agc ggc gac ggc agt ggc agt ggc ggc      830
Tyr Ala Pro Gly Asn Gly Gly Ser Gly Asp Gly Ser Gly Ser Gly Gly
    240                 245                 250

ggt ggc ggg agc gcg tcg cac aca ccg cag ggc agc ggc ggc ttg gag      878
Gly Gly Gly Ser Ala Ser His Thr Pro Gln Gly Ser Gly Gly Leu Glu
255                 260                 265                 270

cac ccg cac ccg ttc gcg tac aag tagctagttc gtacgtcgtt cgacttgagc      932
His Pro His Pro Phe Ala Tyr Lys
                275

aagccatcga tctgctgatc tgaacgtacg ctgtattgta cacgcatgca cgtacgtatc      992
ggcggctagc tctcctgttt aagttgtact gtgattctgt cccggccggc tagcaactta     1052
gtatcttcct tcagtctcta gtttcttagc agtcgtagaa gtgttcaatg cttgccagtg     1112
tgttgtttta gggccggggt aaaccatccg atgagattat ttcaaaaaaa aaaaaaaaaa     1172
a                                                                    1173
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<210> 2
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<212> PRT
<213> Zea mays

<400> 2

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 1               5                  10                  15
Ala Ala Gly Gly Ala Asn Asn Gly Gly Ala Ala Gln Gln His Ala Ala
            20                  25                  30
Pro Ala Ile Arg Glu Gln Asp Arg Leu Met Pro Ile Ala Asn Val Ile
        35                  40                  45
Arg Ile Met Arg Arg Val Leu Pro Ala His Ala Lys Ile Ser Asp Asp
    50                  55                  60
Ala Lys Glu Thr Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Ile
65                  70                  75                  80
Thr Gly Glu Ala Asn Glu Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile
                85                  90                  95
Thr Ala Glu Asp Val Leu Trp Ala Met Ser Arg Leu Gly Phe Asp Asp
            100                 105                 110
Tyr Val Glu Pro Leu Gly Ala Tyr Leu His Arg Tyr Arg Glu Phe Glu
        115                 120                 125
Gly Asp Ala Arg Gly Val Gly Leu Val Pro Gly Ala Ala Pro Ser Arg
    130                 135                 140
Gly Gly Asp His His Pro His Ser Met Ser Pro Ala Ala Met Leu Lys
145                 150                 155                 160
Ser Arg Gly Pro Val Ser Gly Ala Ala Met Leu Pro His His His His
                165                 170                 175
His His Asp Met Gln Met His Ala Ala Met Tyr Gly Gly Thr Ala Val
            180                 185                 190
Pro Pro Pro Ala Gly Pro Pro His His Gly Gly Phe Leu Met Pro His
        195                 200                 205
Pro Gln Gly Ser Ser His Tyr Leu Pro Tyr Ala Tyr Glu Pro Thr Tyr
    210                 215                 220
Gly Gly Glu His Ala Met Ala Ala Tyr Tyr Gly Gly Ala Ala Tyr Ala
225                 230                 235                 240
Pro Gly Asn Gly Gly Ser Gly Asp Gly Ser Gly Ser Gly Gly Gly Gly
                245                 250                 255
Gly Ser Ala Ser His Thr Pro Gln Gly Ser Gly Gly Leu Glu His Pro
            260                 265                 270
His Pro Phe Ala Tyr Lys
        275
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<212> DNA
<213> Artificial Sequence

<220>
<223> primer

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<210> 4
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 4
gccgggacag aatcacagta
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<210> 5

<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 5
tagtagcgag agccaatgga
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<210> 6
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 6
cccggcccta aaacaacaca
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<210> 7
<211> 481
<212> DNA
<213> Argemone mexicana

<220>
<221> CDS
<222> (44)...(481)

<221> misc_feature
<222> (1)...(481)
<223> n = A,T,C or G

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Met Glu Arg Gly
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ggt ggt ggt ggt ggt agt ggt ggt ggt ttc cat gga tat cag aaa ctc 103
Gly Gly Gly Gly Gly Ser Gly Gly Gly Phe His Gly Tyr Gln Lys Leu
5 10 15 20

cca aaa tca aac tcc gct gga atg atg ctc tcg gag cta tcg aat aac 151
Pro Lys Ser Asn Ser Ala Gly Met Met Leu Ser Glu Leu Ser Asn Asn
25 30 35

aac aac aat att gac gta aac tct aca tgt act gta cga gag caa gat 199
Asn Asn Asn Ile Asp Val Asn Ser Thr Cys Thr Val Arg Glu Gln Asp
40 45 50

cga tac atg cca att gct aat gtg atc agg atc atg cgt aag gta ctt 247
Arg Tyr Met Pro Ile Ala Asn Val Ile Arg Ile Met Arg Lys Val Leu
55 60 65

cct act cat gcc aag atc tct gac gat gcc aaa gaa act atc caa gaa 295
Pro Thr His Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr Ile Gln Glu
70 75 80

tgt gtc tca gaa tac atc agt ttc atc aca agt gaa gcc aat gat cgt 343

```
Cys Val Ser Glu Tyr Ile Ser Phe Ile Thr Ser Glu Ala Asn Asp Arg
 85                  90                  95                 100

tgc caa cgt gaa caa aga aag aca atc aca gct gaa gat gtt tta tgg      391
Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp Val Leu Trp
                105                 110                 115

gcg atg agc aaa cta ggg ntt gat gag tac att gaa cct cta act ctt      439
Ala Met Ser Lys Leu Gly Xaa Asp Glu Tyr Ile Glu Pro Leu Thr Leu
            120                 125                 130

tac ctt caa cgt tat cgt gag ttt gaa ggt gna cgt tgg tca              481
Tyr Leu Gln Arg Tyr Arg Glu Phe Glu Gly Xaa Arg Trp Ser
        135                 140                 145
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<210> 8
<211> 146
<212> PRT
<213> Argemone mexicana

<220>
<221> VARIANT
<222> (1)...(146)
<223> Xaa = Any Amino Acid

<400> 8

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Met Glu Arg Gly Gly Gly Gly Gly Gly Ser Gly Gly Gly Phe His Gly
 1               5                  10                  15
Tyr Gln Lys Leu Pro Lys Ser Asn Ser Ala Gly Met Met Leu Ser Glu
            20                  25                  30
Leu Ser Asn Asn Asn Asn Asn Ile Asp Val Asn Ser Thr Cys Thr Val
        35                  40                  45
Arg Glu Gln Asp Arg Tyr Met Pro Ile Ala Asn Val Ile Arg Ile Met
    50                  55                  60
Arg Lys Val Leu Pro Thr His Ala Lys Ile Ser Asp Asp Ala Lys Glu
65                  70                  75                  80
Thr Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Ile Thr Ser Glu
                85                  90                  95
Ala Asn Asp Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu
            100                 105                 110
Asp Val Leu Trp Ala Met Ser Lys Leu Gly Xaa Asp Glu Tyr Ile Glu
        115                 120                 125
Pro Leu Thr Leu Tyr Leu Gln Arg Tyr Arg Glu Phe Glu Gly Xaa Arg
    130                 135                 140
Trp Ser
145
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<210> 9
<211> 942
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (3)...(722)

<400> 9

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gc acg agc tct ctt ata atc aca cac aca cct acc tta ata gct atg      47
   Thr Ser Ser Leu Ile Ile Thr His Thr Pro Thr Leu Ile Ala Met
    1               5                  10                  15
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```
gaa act gga ggc ttt cac ggc tac cgc aag ctc ccc aac acc acc gct          95
Glu Thr Gly Gly Phe His Gly Tyr Arg Lys Leu Pro Asn Thr Thr Ala
                20                  25                  30

ggg ttg aag ctg tca gtg tca gac atg aac atg agg cag cag gta gca         143
Gly Leu Lys Leu Ser Val Ser Asp Met Asn Met Arg Gln Gln Val Ala
            35                  40                  45

tca tca gat cac agt gca gcc aca gga gag gag aac gaa tgc acg gtg         191
Ser Ser Asp His Ser Ala Ala Thr Gly Glu Glu Asn Glu Cys Thr Val
        50                  55                  60

agg gag caa gac agg ttc atg cca atc gcc aac gtg att agg atc atg         239
Arg Glu Gln Asp Arg Phe Met Pro Ile Ala Asn Val Ile Arg Ile Met
    65                  70                  75

cgc aag att ctc cct cca cac gca aaa atc tcg gac gat gca aaa gaa         287
Arg Lys Ile Leu Pro Pro His Ala Lys Ile Ser Asp Asp Ala Lys Glu
80                  85                  90                  95

aca atc caa gag tgc gtg tct gag tac atc agc ttc atc aca ggt gag         335
Thr Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Ile Thr Gly Glu
                100                 105                 110

gcg aac gag cgt tgc cag agg gag cag cgg aag acc ata acc gca gag         383
Ala Asn Glu Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu
            115                 120                 125

gac gtg ctt tgg gcc atg agc aag ctt gga ttc gac gac tac atc gaa         431
Asp Val Leu Trp Ala Met Ser Lys Leu Gly Phe Asp Asp Tyr Ile Glu
        130                 135                 140

ccg ttg acc atg tac ctt cac cgc tac cgt gaa ctt gag ggt gac cgc         479
Pro Leu Thr Met Tyr Leu His Arg Tyr Arg Glu Leu Glu Gly Asp Arg
    145                 150                 155

acc tct atg agg ggt gaa cca ctc ggg aag agg act gtg gaa tac gcc         527
Thr Ser Met Arg Gly Glu Pro Leu Gly Lys Arg Thr Val Glu Tyr Ala
160                 165                 170                 175

acg ctt ggt gtt gct act gct ttt gtc cct cca ccc tat cat cac cac         575
Thr Leu Gly Val Ala Thr Ala Phe Val Pro Pro Pro Tyr His His His
                180                 185                 190

aat ggg tac ttt ggt gct gcc atg ccc atg ggg act tac gtt agg gaa         623
Asn Gly Tyr Phe Gly Ala Ala Met Pro Met Gly Thr Tyr Val Arg Glu
            195                 200                 205

gcg cca cca aat aca gcc tcc tcc cat cac cac cac cac cac cac cac         671
Ala Pro Pro Asn Thr Ala Ser Ser His His His His His His His His
        210                 215                 220

cac cat gct cgt gga atc tcc aat gct cat gaa cca aat gct cgc tcc         719
His His Ala Arg Gly Ile Ser Asn Ala His Glu Pro Asn Ala Arg Ser
    225                 230                 235

ata taaaattata taattatgac taggattcag aacaagactt gatgatgatt              772
Ile
240

agcttaactc tcagtaattg gtgctagagt actactgttg ttgaggatac tttattttat       832
aattaagggc tgggaaggga gttagtatat tcctaatcct aactatgtgc atctttaatt       892
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tatgaaatca ctttgtttta acctttgatg aaaaaaaaaa aaaaaaaaaa 942

<210> 10
<211> 240
<212> PRT
<213> Glycine max

<400> 10

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Thr Ser Ser Leu Ile Ile Thr His Thr Pro Thr Leu Ile Ala Met Glu
 1               5                  10                  15
Thr Gly Gly Phe His Gly Tyr Arg Lys Leu Pro Asn Thr Thr Ala Gly
            20                  25                  30
Leu Lys Leu Ser Val Ser Asp Met Asn Met Arg Gln Gln Val Ala Ser
        35                  40                  45
Ser Asp His Ser Ala Ala Thr Gly Glu Glu Asn Glu Cys Thr Val Arg
    50                  55                  60
Glu Gln Asp Arg Phe Met Pro Ile Ala Asn Val Ile Arg Ile Met Arg
65                  70                  75                  80
Lys Ile Leu Pro Pro His Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr
                85                  90                  95
Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Ile Thr Gly Glu Ala
            100                 105                 110
Asn Glu Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp
        115                 120                 125
Val Leu Trp Ala Met Ser Lys Leu Gly Phe Asp Asp Tyr Ile Glu Pro
    130                 135                 140
Leu Thr Met Tyr Leu His Arg Tyr Arg Glu Leu Glu Gly Asp Arg Thr
145                 150                 155                 160
Ser Met Arg Gly Glu Pro Leu Gly Lys Arg Thr Val Glu Tyr Ala Thr
                165                 170                 175
Leu Gly Val Ala Thr Ala Phe Val Pro Pro Pro Tyr His His His Asn
            180                 185                 190
Gly Tyr Phe Gly Ala Ala Met Pro Met Gly Thr Tyr Val Arg Glu Ala
        195                 200                 205
Pro Pro Asn Thr Ala Ser Ser His His His His His His His His His
    210                 215                 220
His Ala Arg Gly Ile Ser Asn Ala His Glu Pro Asn Ala Arg Ser Ile
225                 230                 235                 240
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<210> 11
<211> 905
<212> DNA
<213> Veronia mespilifolia

<220>
<221> CDS
<222> (58)...(699)

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Met
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gaa cgt gga gga ggt ttc cat ggc tac cac agg ctc ccc atc cac cct 108
Glu Arg Gly Gly Gly Phe His Gly Tyr His Arg Leu Pro Ile His Pro
5 10 15

aca tct gga atc caa caa tcg gat atg aag cta aag cta cca gaa atg 156
Thr Ser Gly Ile Gln Gln Ser Asp Met Lys Leu Lys Leu Pro Glu Met
20 25 30

```
acc aac aat aac tcg tcc act gat gac aat gag tgc acc gtt cga gaa      204
Thr Asn Asn Asn Ser Ser Thr Asp Asp Asn Glu Cys Thr Val Arg Glu
     35                  40                  45

cag gac cgc ttc atg ccg ata gca aac gtg atc cgc atc atg cgg aag      252
Gln Asp Arg Phe Met Pro Ile Ala Asn Val Ile Arg Ile Met Arg Lys
 50                  55                  60                  65

atc ctt cct cca cat gcc aag atc tct gat gat gcc aaa gag acg atc      300
Ile Leu Pro Pro His Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr Ile
                 70                  75                  80

caa gaa tgt gtt tca gag tac att agc ttt gtc aca ggc gag gca aat      348
Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Val Thr Gly Glu Ala Asn
             85                  90                  95

gac cgc tgc cag cgt gag caa agg aag acc atc aca gct gaa gat gtg      396
Asp Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp Val
        100                 105                 110

ctc tgg gct atg agc aaa ctg gga ttt gat gat tat atc gag ccc ttg      444
Leu Trp Ala Met Ser Lys Leu Gly Phe Asp Asp Tyr Ile Glu Pro Leu
    115                 120                 125

act gtg tat ctc cat cgc tac agg gag ttt gat ggt ggc gaa cgt gga      492
Thr Val Tyr Leu His Arg Tyr Arg Glu Phe Asp Gly Gly Glu Arg Gly
130                 135                 140                 145

tcc ata agg ggt gag ccc ctt gtg aag agg agt act tct gat cct ggt      540
Ser Ile Arg Gly Glu Pro Leu Val Lys Arg Ser Thr Ser Asp Pro Gly
                150                 155                 160

cac ttt ggg atg gct tct ttt gtg cct gct ttt cat atg ggt cat cat      588
His Phe Gly Met Ala Ser Phe Val Pro Ala Phe His Met Gly His His
            165                 170                 175

aac ggc ttc ttt ggt cct gca agc att ggt ggt ttc ctg aaa gac cca      636
Asn Gly Phe Phe Gly Pro Ala Ser Ile Gly Gly Phe Leu Lys Asp Pro
        180                 185                 190

tcg agt gct ggc cct tcg gga cct gca gtc gct ggg ttt gag ccg tat      684
Ser Ser Ala Gly Pro Ser Gly Pro Ala Val Ala Gly Phe Glu Pro Tyr
    195                 200                 205

gct cag tgt aaa gag taactgcaaa aagtaggggt tgggatgaga tgatgatgat      739
Ala Gln Cys Lys Glu
210

ggtggtggtg gtggtggttt gttttgtttt gttctttctt ttttttttct tctttctttt     799
cttggtcatt gaggaacaaa cttacattgg ttcactttgg ctaggcatgt aaacggttaa     859
catgcttatc aagtagtagt tttcgatcaa aaaaaaaaaa aaaaaa                    905
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<210> 12
<211> 214
<212> PRT
<213> Veronia mespilifolia

<400> 12

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Met Glu Arg Gly Gly Gly Phe His Gly Tyr His Arg Leu Pro Ile His
 1               5                  10                  15
Pro Thr Ser Gly Ile Gln Gln Ser Asp Met Lys Leu Lys Leu Pro Glu
            20                  25                  30
```

```
Met Thr Asn Asn Asn Ser Ser Thr Asp Asp Asn Glu Cys Thr Val Arg
        35                  40                  45
Glu Gln Asp Arg Phe Met Pro Ile Ala Asn Val Ile Arg Ile Met Arg
    50                  55                  60
Lys Ile Leu Pro Pro His Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr
65                  70                  75                  80
Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Val Thr Gly Glu Ala
                85                  90                  95
Asn Asp Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp
            100                 105                 110
Val Leu Trp Ala Met Ser Lys Leu Gly Phe Asp Asp Tyr Ile Glu Pro
        115                 120                 125
Leu Thr Val Tyr Leu His Arg Tyr Arg Glu Phe Asp Gly Gly Glu Arg
    130                 135                 140
Gly Ser Ile Arg Gly Glu Pro Leu Val Lys Arg Ser Thr Ser Asp Pro
145                 150                 155                 160
Gly His Phe Gly Met Ala Ser Phe Val Pro Ala Phe His Met Gly His
                165                 170                 175
His Asn Gly Phe Phe Gly Pro Ala Ser Ile Gly Gly Phe Leu Lys Asp
            180                 185                 190
Pro Ser Ser Ala Gly Pro Ser Gly Pro Ala Val Ala Gly Phe Glu Pro
        195                 200                 205
Tyr Ala Gln Cys Lys Glu
    210
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<210> 13
<211> 763
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (1)...(480)

<400> 13

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gca cga ggc aag acc gtc acc tcc gag gac atc gtg tgg gcc atg agc        48
Ala Arg Gly Lys Thr Val Thr Ser Glu Asp Ile Val Trp Ala Met Ser
 1               5                  10                  15

cgc ctc ggc ttc gac gac tac gtc gcg ccc ctc ggc gcc ttc ctc cag        96
Arg Leu Gly Phe Asp Asp Tyr Val Ala Pro Leu Gly Ala Phe Leu Gln
            20                  25                  30

cgc atg cgc gac gac agc gac cac ggc ggt gaa gag cgc ggc ggc cct       144
Arg Met Arg Asp Asp Ser Asp His Gly Gly Glu Glu Arg Gly Gly Pro
        35                  40                  45

gca ggg cgt ggt ggc tcg cgc cgc ggc tcg tcg tcc ttg ccg ctc cac       192
Ala Gly Arg Gly Gly Ser Arg Arg Gly Ser Ser Ser Leu Pro Leu His
    50                  55                  60

tgc ccg cag cag atg cac cac ctg cac cca gcc gtc tgc cgg cgt ccg       240
Cys Pro Gln Gln Met His His Leu His Pro Ala Val Cys Arg Arg Pro
65                  70                  75                  80

cac cag agc gtg tcg cct gct gca gga tac gcc gtc cgg ccc gtt ccc       288
His Gln Ser Val Ser Pro Ala Ala Gly Tyr Ala Val Arg Pro Val Pro
                85                  90                  95

cgc ccg atg cca gcc cgt ggg tac cgc atg cag ggc gga gac cac cgc       336
Arg Pro Met Pro Ala Arg Gly Tyr Arg Met Gln Gly Gly Asp His Arg
            100                 105                 110
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agc gtg ggc ggc gtg gct ccc tgc agc tac gga ggg gcg ctc gtc cag      384
Ser Val Gly Gly Val Ala Pro Cys Ser Tyr Gly Gly Ala Leu Val Gln
        115                 120                 125

gcc ggt gga acc caa cac gtt gtt gga ttc cac gac gac gag gca agc      432
Ala Gly Gly Thr Gln His Val Val Gly Phe His Asp Asp Glu Ala Ser
    130                 135                 140

tct tcg agt gaa aat ccg ccg ccg gag ggg cgt gcc gct ggc tcg aac      480
Ser Ser Ser Glu Asn Pro Pro Pro Glu Gly Arg Ala Ala Gly Ser Asn
145                 150                 155                 160

tagcctagct tctcagttcc ccgtgtacaa taagaggggc ggtcgcggcg ccgcgccgcg    540
cccttgggtt gggccgggcg ctatgctgca gtttggtttg taaactaacg agcctagggt    600
agctggtgca cgcgcgccac ctcgccggac gtcgccgtcg tcgtcggcat ggacttaacc    660
ggcgggccct gttgttattt ctcaagtttg tagccaacgc actgttcggt gcgttccata    720
atttaattta ccatgttgct ctcgaaaaaa aaaaaaaaaa aaa                      763

      <210> 14
      <211> 160
      <212> PRT
      <213> Zea mays

      <400> 14
Ala Arg Gly Lys Thr Val Thr Ser Glu Asp Ile Val Trp Ala Met Ser
 1               5                  10                  15
Arg Leu Gly Phe Asp Asp Tyr Val Ala Pro Leu Gly Ala Phe Leu Gln
            20                  25                  30
Arg Met Arg Asp Asp Ser Asp His Gly Gly Glu Glu Arg Gly Gly Pro
        35                  40                  45
Ala Gly Arg Gly Gly Ser Arg Arg Gly Ser Ser Ser Leu Pro Leu His
    50                  55                  60
Cys Pro Gln Gln Met His His Leu His Pro Ala Val Cys Arg Arg Pro
65                  70                  75                  80
His Gln Ser Val Ser Pro Ala Ala Gly Tyr Ala Val Arg Pro Val Pro
                85                  90                  95
Arg Pro Met Pro Ala Arg Gly Tyr Arg Met Gln Gly Gly Asp His Arg
            100                 105                 110
Ser Val Gly Gly Val Ala Pro Cys Ser Tyr Gly Gly Ala Leu Val Gln
        115                 120                 125
Ala Gly Gly Thr Gln His Val Val Gly Phe His Asp Asp Glu Ala Ser
    130                 135                 140
Ser Ser Ser Glu Asn Pro Pro Pro Glu Gly Arg Ala Ala Gly Ser Asn
145                 150                 155                 160

      <210> 15
      <211> 622
      <212> DNA
      <213> Zea mays

      <220>
      <221> CDS
      <222> (3)...(622)

      <221> misc_feature
      <222> (1)...(622)
      <223> n = A,T,C or G

      <400> 15
gc atg aat aat ccc caa aac cct aaa gcc agt gct cct tgc acc ttg       47
  Met Asn Asn Pro Gln Asn Pro Lys Ala Ser Ala Pro Cys Thr Leu
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```
    1               5                  10                  15

cca ccg gag ctt ccc aaa gaa gca gtg gcg acc gac gaa gca ccg ccg        95
Pro Pro Glu Leu Pro Lys Glu Ala Val Ala Thr Asp Glu Ala Pro Pro
                20                  25                  30

cca atg ggc aac aac aac aac acg gaa tcg gcg acg gcg acg atg gtc       143
Pro Met Gly Asn Asn Asn Asn Thr Glu Ser Ala Thr Ala Thr Met Val
            35                  40                  45

cgg gag cag gac cgg ctg atg ccc gtg gcc aac gtg tcc cgc atc atg       191
Arg Glu Gln Asp Arg Leu Met Pro Val Ala Asn Val Ser Arg Ile Met
        50                  55                  60

cgc caa gtg ctg cct ccg tac gcc aag atc tcc gac gac gcc can gaa       239
Arg Gln Val Leu Pro Pro Tyr Ala Lys Ile Ser Asp Asp Ala Xaa Glu
    65                  70                  75

gtn atc caa gaa ttg ctn ttc gga att tca tca ctt ncg tcc tgg cga       287
Xaa Ile Gln Glu Leu Xaa Phe Gly Ile Ser Ser Leu Xaa Ser Trp Arg
80                  85                  90                  95

ggc gaa acg aag cgg tgc cac acc gag cgc cgc aag acc gtc acc tcc       335
Gly Glu Thr Lys Arg Cys His Thr Glu Arg Arg Lys Thr Val Thr Ser
                100                 105                 110

gaa gac atc gtg tgg gcc atg agc cgc ctc ggc ttc gac gac tac gtc       383
Glu Asp Ile Val Trp Ala Met Ser Arg Leu Gly Phe Asp Asp Tyr Val
            115                 120                 125

gcg ccc ctc ggc gcc ttc ctc cag cgc atg cgc gac nac agc gaa cac       431
Ala Pro Leu Gly Ala Phe Leu Gln Arg Met Arg Asp Xaa Ser Glu His
        130                 135                 140

ggg ggt gaa aac gcg gcg gcc tgc ang ggg tng tgg tcn cgc cgc ggg       479
Gly Gly Glu Asn Ala Ala Ala Cys Xaa Gly Xaa Trp Xaa Arg Arg Gly
    145                 150                 155

tcg tct nct tgg cgc tcc ctt gcc gca ana gat gac aac ttg cac caa       527
Ser Ser Xaa Trp Arg Ser Leu Ala Ala Xaa Asp Asp Asn Leu His Gln
160                 165                 170                 175

acg tct gcc ggg ntc gga cca aaa ctn ttc cct gtt gca gga ata ccc       575
Thr Ser Ala Gly Xaa Gly Pro Lys Xaa Phe Pro Val Ala Gly Ile Pro
                180                 185                 190

gtc cng ggc cnt tcc ccc ccn aat cca acc att tgg ttt ccc ctt gc        622
Val Xaa Gly Xaa Ser Pro Xaa Asn Pro Thr Ile Trp Phe Pro Leu
            195                 200                 205
```

<210> 16
<211> 206
<212> PRT
<213> Zea mays

<220>
<221> VARIANT
<222> (1)...(206)
<223> Xaa = Any Amino Acid

<400> 16

```
Met Asn Asn Pro Gln Asn Pro Lys Ala Ser Ala Pro Cys Thr Leu Pro
 1               5                  10                  15
Pro Glu Leu Pro Lys Glu Ala Val Ala Thr Asp Glu Ala Pro Pro Pro
            20                  25                  30
Met Gly Asn Asn Asn Asn Thr Glu Ser Ala Thr Ala Thr Met Val Arg
        35                  40                  45
Glu Gln Asp Arg Leu Met Pro Val Ala Asn Val Ser Arg Ile Met Arg
    50                  55                  60
Gln Val Leu Pro Pro Tyr Ala Lys Ile Ser Asp Asp Ala Xaa Glu Xaa
65                  70                  75                  80
Ile Gln Glu Leu Xaa Phe Gly Ile Ser Ser Leu Xaa Ser Trp Arg Gly
                85                  90                  95
Glu Thr Lys Arg Cys His Thr Glu Arg Arg Lys Thr Val Thr Ser Glu
            100                 105                 110
Asp Ile Val Trp Ala Met Ser Arg Leu Gly Phe Asp Asp Tyr Val Ala
        115                 120                 125
Pro Leu Gly Ala Phe Leu Gln Arg Met Arg Asp Xaa Ser Glu His Gly
    130                 135                 140
Gly Glu Asn Ala Ala Ala Cys Xaa Gly Xaa Trp Xaa Arg Arg Gly Ser
145                 150                 155                 160
Ser Xaa Trp Arg Ser Leu Ala Ala Xaa Asp Asp Asn Leu His Gln Thr
                165                 170                 175
Ser Ala Gly Xaa Gly Pro Lys Xaa Phe Pro Val Ala Gly Ile Pro Val
            180                 185                 190
Xaa Gly Xaa Ser Pro Xaa Asn Pro Thr Ile Trp Phe Pro Leu
        195                 200                 205
```

<210> 17
<211> 1121
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (3)...(1121)

<400> 17

```
gc acg agg gaa act gga ggc ttt cat ggc tac cgc aag ctc ccc aac      47
   Thr Arg Glu Thr Gly Gly Phe His Gly Tyr Arg Lys Leu Pro Asn
    1               5                  10                  15

aca acc tct ggg ttg aag ctg tca gtg tca gac atg aac atg aac atg      95
Thr Thr Ser Gly Leu Lys Leu Ser Val Ser Asp Met Asn Met Asn Met
                20                  25                  30

agg cag cag cag gta gca tca tca gat cag aac tgc agc aac cac agt     143
Arg Gln Gln Gln Val Ala Ser Ser Asp Gln Asn Cys Ser Asn His Ser
            35                  40                  45

gca gca gga gag gag aac gaa tgc acg gtg agg gag caa gac agg ttc     191
Ala Ala Gly Glu Glu Asn Glu Cys Thr Val Arg Glu Gln Asp Arg Phe
        50                  55                  60

atg cca atc gct aac gtg ata cgg atc atg cgc aag att ctc cct cca     239
Met Pro Ile Ala Asn Val Ile Arg Ile Met Arg Lys Ile Leu Pro Pro
    65                  70                  75

cac gca aaa atc tcc gat gat gca aag gag aca atc caa gag tgc gtg     287
His Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr Ile Gln Glu Cys Val
80                  85                  90                  95

tcg gag tac atc agc ttc atc acc ggg gag gcc aac gag cgt tgc cag     335
```

```
Ser Glu Tyr Ile Ser Phe Ile Thr Gly Glu Ala Asn Glu Arg Cys Gln
                100                 105                 110

agg gag cag cgc aag acc ata acc gca gag gac gtg ctt tgg gca atg      383
Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp Val Leu Trp Ala Met
            115                 120                 125

agt aag ctt gga ttc gac gac tac atc gaa ccg tta acc atg tac ctt      431
Ser Lys Leu Gly Phe Asp Asp Tyr Ile Glu Pro Leu Thr Met Tyr Leu
        130                 135                 140

cac cgc tac cgt gag ctg gag ggt gac cgc acc tct atg agg ggt gaa      479
His Arg Tyr Arg Glu Leu Glu Gly Asp Arg Thr Ser Met Arg Gly Glu
    145                 150                 155

ccg ctc ggg aag agg act gtg gaa tat gcc acg ctt gct act gct ttt      527
Pro Leu Gly Lys Arg Thr Val Glu Tyr Ala Thr Leu Ala Thr Ala Phe
160                 165                 170                 175

gtg ccg cca ccc ttt cat cac cac aat ggc tac ttt ggt gct gcc atg      575
Val Pro Pro Pro Phe His His His Asn Gly Tyr Phe Gly Ala Ala Met
                180                 185                 190

ccc atg ggg act tac gtt agg gaa acg cca cca aat gct gcg tca tct      623
Pro Met Gly Thr Tyr Val Arg Glu Thr Pro Pro Asn Ala Ala Ser Ser
            195                 200                 205

cat cac cat cat gga atc tcc aat gct cat gaa cca aat gct cgc tcc      671
His His His His Gly Ile Ser Asn Ala His Glu Pro Asn Ala Arg Ser
        210                 215                 220

ata taa aat taa tga aga gta ctg ttc agt agg aga aca aga ctt ctt      719
Ile  *  Asn  *   *  Arg Val Leu Phe Ser Arg Arg Thr Arg Leu Leu
    225                 230                 235

gga ctt gat tag ctt aac tct cag tga ttg gtg tta gag tac tgt tgt      767
Gly Leu Asp  *  Leu Asn Ser Gln  *  Leu Val Leu Glu Tyr Cys Cys
                240                 245                 250

tga gga tgg tta att tta taa tta agg gct ggg aat tgg gga gtt agt      815
 *  Gly Trp Leu Ile Leu  *  Leu Arg Ala Gly Asn Trp Gly Val Ser
            255                 260

ata tat tcc taa tcc taa tta tgt gca tct tta att tat gga ata act      863
Ile Tyr Ser  *  Ser  *  Leu Cys Ala Ser Leu Ile Tyr Gly Ile Thr
265                 270                 275

ttg ttt ttt gtt tta act tct gat aat ttg gat ttt ctg atg ttt aat      911
Leu Phe Phe Val Leu Thr Ser Asp Asn Leu Asp Phe Leu Met Phe Asn
    280                 285                 290

gtg gtt ttg tct atc cct tat taa cag tgc caa gct taa ggt ttt agc      959
Val Val Leu Ser Ile Pro Tyr  *  Gln Cys Gln Ala  *  Gly Phe Ser
295                 300                 305

cat gct cca aaa tgg aat act tgt act gtt atg ttg ttc tgg tag tga     1007
His Ala Pro Lys Trp Asn Thr Cys Thr Val Met Leu Phe Trp  *   *
    310                 315                 320

tgg tga tga aac ctg caa gtt atg ttt atg tat aaa gcc act att gat     1055
Trp  *   *  Asn Leu Gln Val Met Phe Met Tyr Lys Ala Thr Ile Asp
                325                 330                 335
```

```
caa aat tag aga aat tat cat tta ata agt atc ctc cca tgt taa ttt      1103
Gln Asn  *  Arg Asn Tyr His Leu Ile Ser Ile Leu Pro Cys  *  Phe
                340                 345                     350

taa aaa aaa aaa aaa aaa                                          1121
 *  Lys Lys Lys Lys Lys
                355
```

<210> 18
<211> 355
<212> PRT
<213> Glycine max

<400> 18

```
Thr Arg Glu Thr Gly Gly Phe His Gly Tyr Arg Lys Leu Pro Asn Thr
 1               5                  10                  15
Thr Ser Gly Leu Lys Leu Ser Val Ser Asp Met Asn Met Asn Met Arg
            20                  25                  30
Gln Gln Gln Val Ala Ser Ser Asp Gln Asn Cys Ser Asn His Ser Ala
        35                  40                  45
Ala Gly Glu Glu Asn Glu Cys Thr Val Arg Glu Gln Asp Arg Phe Met
    50                  55                  60
Pro Ile Ala Asn Val Ile Arg Ile Met Arg Lys Ile Leu Pro Pro His
65                  70                  75                  80
Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr Ile Gln Glu Cys Val Ser
                85                  90                  95
Glu Tyr Ile Ser Phe Ile Thr Gly Glu Ala Asn Glu Arg Cys Gln Arg
            100                 105                 110
Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp Val Leu Trp Ala Met Ser
        115                 120                 125
Lys Leu Gly Phe Asp Asp Tyr Ile Glu Pro Leu Thr Met Tyr Leu His
    130                 135                 140
Arg Tyr Arg Glu Leu Glu Gly Asp Arg Thr Ser Met Arg Gly Glu Pro
145                 150                 155                 160
Leu Gly Lys Arg Thr Val Glu Tyr Ala Thr Leu Ala Thr Ala Phe Val
                165                 170                 175
Pro Pro Pro Phe His His His Asn Gly Tyr Phe Gly Ala Ala Met Pro
            180                 185                 190
Met Gly Thr Tyr Val Arg Glu Thr Pro Pro Asn Ala Ala Ser Ser His
        195                 200                 205
His His His Gly Ile Ser Asn Ala His Glu Pro Asn Ala Arg Ser Ile
    210                 215                 220
Asn Arg Val Leu Phe Ser Arg Arg Thr Arg Leu Leu Gly Leu Asp Leu
225                 230                 235                 240
Asn Ser Gln Leu Val Leu Glu Tyr Cys Cys Gly Trp Leu Ile Leu Leu
                245                 250                 255
Arg Ala Gly Asn Trp Gly Val Ser Ile Tyr Ser Ser Leu Cys Ala Ser
            260                 265                 270
Leu Ile Tyr Gly Ile Thr Leu Phe Phe Val Leu Thr Ser Asp Asn Leu
        275                 280                 285
Asp Phe Leu Met Phe Asn Val Val Leu Ser Ile Pro Tyr Gln Cys Gln
    290                 295                 300
Ala Gly Phe Ser His Ala Pro Lys Trp Asn Thr Cys Thr Val Met Leu
305                 310                 315                 320
Phe Trp Trp Asn Leu Gln Val Met Phe Met Tyr Lys Ala Thr Ile Asp
                325                 330                 335
Gln Asn Arg Asn Tyr His Leu Ile Ser Ile Leu Pro Cys Phe Lys Lys
            340                 345                 350
Lys Lys Lys
        355
```

<210> 19
<211> 796
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (1)...(513)

<400> 19

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gca cga gca atg gcg gga gtg agg gaa cag gac cag tac atg ccg ata        48
Ala Arg Ala Met Ala Gly Val Arg Glu Gln Asp Gln Tyr Met Pro Ile
 1               5                  10                  15

gcg aac gtg ata agg atc atg cgt cgg att ctg cca gcg cac gcg aag        96
Ala Asn Val Ile Arg Ile Met Arg Arg Ile Leu Pro Ala His Ala Lys
            20                  25                  30

atc tca gac gac gcg aag gag acg atc cag gag tgc gtg tct gag tac       144
Ile Ser Asp Asp Ala Lys Glu Thr Ile Gln Glu Cys Val Ser Glu Tyr
        35                  40                  45

atc agt ttc atc acg gcg gag gcg aac gag cgg tgc cag cgg gag cag       192
Ile Ser Phe Ile Thr Ala Glu Ala Asn Glu Arg Cys Gln Arg Glu Gln
    50                  55                  60

cgg aag acg gtg acc gca gag gat gtg ttg tgg gcg atg gag aag ctt       240
Arg Lys Thr Val Thr Ala Glu Asp Val Leu Trp Ala Met Glu Lys Leu
65                  70                  75                  80

ggc ttt gac aac tac gct cac cct ctc tct ctt tac ctt cac cgc tac       288
Gly Phe Asp Asn Tyr Ala His Pro Leu Ser Leu Tyr Leu His Arg Tyr
                85                  90                  95

cgc gag agt gaa gga gaa cct gct tct gtc aga cgc gct tct tct gca       336
Arg Glu Ser Glu Gly Glu Pro Ala Ser Val Arg Arg Ala Ser Ser Ala
            100                 105                 110

atg ggg atc aat aat aat atg gtg cac cca cct tat att aat tct cat       384
Met Gly Ile Asn Asn Asn Met Val His Pro Pro Tyr Ile Asn Ser His
        115                 120                 125

ggc ttt gga atg ttt gat ttt gac cca tca tcg caa ggg ttt tac agg       432
Gly Phe Gly Met Phe Asp Phe Asp Pro Ser Ser Gln Gly Phe Tyr Arg
    130                 135                 140

gac gat cat aac gct gct tct gga tct ggt ggt ttt gtt gcg cct ttt       480
Asp Asp His Asn Ala Ala Ser Gly Ser Gly Gly Phe Val Ala Pro Phe
145                 150                 155                 160

gat cct tat gct aac atc aaa cgt gat gcc ctg tgatcatgta agaacaacaa      533
Asp Pro Tyr Ala Asn Ile Lys Arg Asp Ala Leu
                165                 170

ctagtgcatg ctgctttttc acttggttag ttatattcaa gcacaagcac atgcaggtgc      593
agctgcaact atttagcttc atctacaaat ctttttttcct ctcttcttct catgctttaa     653
ttatttagag acaatacttg ttattcattg ttatgctcaa ttgctagctt ctattcatcg      713
tcgactgtct gtattgttga tgttcattac agtaacagat aagatggtaa ctgctttact      773
acttcaaaaa aaaaaaaaaa aaa                                              796
```

<210> 20

<211> 171
<212> PRT
<213> Glycine max

<400> 20

```
Ala Arg Ala Met Ala Gly Val Arg Glu Gln Asp Gln Tyr Met Pro Ile
 1               5                  10                  15
Ala Asn Val Ile Arg Ile Met Arg Arg Ile Leu Pro Ala His Ala Lys
            20                  25                  30
Ile Ser Asp Asp Ala Lys Glu Thr Ile Gln Glu Cys Val Ser Glu Tyr
        35                  40                  45
Ile Ser Phe Ile Thr Ala Glu Ala Asn Glu Arg Cys Gln Arg Glu Gln
    50                  55                  60
Arg Lys Thr Val Thr Ala Glu Asp Val Leu Trp Ala Met Glu Lys Leu
65                  70                  75                  80
Gly Phe Asp Asn Tyr Ala His Pro Leu Ser Leu Tyr Leu His Arg Tyr
                85                  90                  95
Arg Glu Ser Glu Gly Glu Pro Ala Ser Val Arg Arg Ala Ser Ser Ala
            100                 105                 110
Met Gly Ile Asn Asn Asn Met Val His Pro Pro Tyr Ile Asn Ser His
        115                 120                 125
Gly Phe Gly Met Phe Asp Phe Asp Pro Ser Ser Gln Gly Phe Tyr Arg
    130                 135                 140
Asp Asp His Asn Ala Ala Ser Gly Ser Gly Gly Phe Val Ala Pro Phe
145                 150                 155                 160
Asp Pro Tyr Ala Asn Ile Lys Arg Asp Ala Leu
                165                 170
```

<210> 21
<211> 1098
<212> DNA
<213> Triticum aestivum

<220>
<221> CDS
<222> (55)...(894)

<400> 21

```
gcacgagcaa gtgcgagtgc gactacctgc attgcacctt ggctagccct agac atg        57
                                                            Met
                                                             1

gag aac gac ggc gtc ccc aac gga cca gcg gcg ccg gca cct acc cag       105
Glu Asn Asp Gly Val Pro Asn Gly Pro Ala Ala Pro Ala Pro Thr Gln
  5                  10                  15

ggg acg ccg gtg gtg cgg gag cag gac cgg ctg atg ccg atc gcg aac       153
Gly Thr Pro Val Val Arg Glu Gln Asp Arg Leu Met Pro Ile Ala Asn
        20                  25                  30

gtg atc cgc atc atg cgc cgt gcg ctc cct gcc cac gcc aag atc tcc       201
Val Ile Arg Ile Met Arg Arg Ala Leu Pro Ala His Ala Lys Ile Ser
    35                  40                  45

gac gac gcc aag gag gcg att cag gaa tgc gtg tcc gag ttc atc agc       249
Asp Asp Ala Lys Glu Ala Ile Gln Glu Cys Val Ser Glu Phe Ile Ser
50                  55                  60                  65

ttc gtc acc ggc gag gcc aac gaa cgg tgc cgc atg cag cac cgc aag       297
Phe Val Thr Gly Glu Ala Asn Glu Arg Cys Arg Met Gln His Arg Lys
                70                  75                  80
```

```
acc gtc aac gcc gaa gac atc gtg tgg gcc cta aac cgc ctc ggc ttc      345
Thr Val Asn Ala Glu Asp Ile Val Trp Ala Leu Asn Arg Leu Gly Phe
                85                  90                  95

gac gac tac gtc gtg ccc ctc agc gtc ttc ctg cac cgc atg cgc gac      393
Asp Asp Tyr Val Val Pro Leu Ser Val Phe Leu His Arg Met Arg Asp
            100                 105                 110

ccc gag gcg ggg aca ggt ggt gcc gct gca ggc gac agc cgc gcc gtg      441
Pro Glu Ala Gly Thr Gly Gly Ala Ala Ala Gly Asp Ser Arg Ala Val
        115                 120                 125

acg agt gcg cct ccc cgc gcg gcc ccg ccc gtg atc cac gcc gtg ccg      489
Thr Ser Ala Pro Pro Arg Ala Ala Pro Pro Val Ile His Ala Val Pro
130                 135                 140                 145

ctg cag gct cag cgc ccg atg tac gcg ccc ccg gct ccg ttg cag gtt      537
Leu Gln Ala Gln Arg Pro Met Tyr Ala Pro Pro Ala Pro Leu Gln Val
                150                 155                 160

gag aat cag atg cag cgg cct gtg tac gct ccc ccg gct ccg gtg cag      585
Glu Asn Gln Met Gln Arg Pro Val Tyr Ala Pro Pro Ala Pro Val Gln
            165                 170                 175

gtt cag atg cag cgg ggc atc tat ggg ccc cgg gct cca gtg cac ggg      633
Val Gln Met Gln Arg Gly Ile Tyr Gly Pro Arg Ala Pro Val His Gly
        180                 185                 190

tac gcc gtc gga atg gcg ccc gtg cgg gcc aac gtc ggc ggg cag tac      681
Tyr Ala Val Gly Met Ala Pro Val Arg Ala Asn Val Gly Gly Gln Tyr
    195                 200                 205

cag gtg ttc ggc gga gag ggt gtc atg gcc cag caa tac tac ggg tac      729
Gln Val Phe Gly Gly Glu Gly Val Met Ala Gln Gln Tyr Tyr Gly Tyr
210                 215                 220                 225

ggg tac gag gaa gga gcg tac ggc gca ggt agc agc aac gga gga gcc      777
Gly Tyr Glu Glu Gly Ala Tyr Gly Ala Gly Ser Ser Asn Gly Gly Ala
                230                 235                 240

gcc att ggc gac gag gag agc tcg tcc aac ggc gtg ccg gca ccg ggg      825
Ala Ile Gly Asp Glu Glu Ser Ser Ser Asn Gly Val Pro Ala Pro Gly
            245                 250                 255

gag ggc atg ggg gag cca gag cca gag cca gca gca gaa gaa tcg cat      873
Glu Gly Met Gly Glu Pro Glu Pro Glu Pro Ala Ala Glu Glu Ser His
        260                 265                 270

gac aag ccc gtc caa tct ggc tagtcgcgtg cgcggcgcgc gttagcttct        924
Asp Lys Pro Val Gln Ser Gly
    275                 280

gcgtcctgtg tactgtaata atttgccgtg tcgatccggc catggtttgt gtgtgcgtag    984
tgcttatcta atgtgggctt gtcctctagt aattcatgta ttgcttatct aatgtggact   1044
tgtcctctag taattcatgt actctttgct gttgaaaaaa aaaaaaaaaa aaaa         1098
```

<210> 22
<211> 280
<212> PRT
<213> Triticum aestivum

<400> 22

```
Met Glu Asn Asp Gly Val Pro Asn Gly Pro Ala Ala Pro Ala Pro Thr
 1               5                  10                  15
Gln Gly Thr Pro Val Val Arg Glu Gln Asp Arg Leu Met Pro Ile Ala
            20                  25                  30
Asn Val Ile Arg Ile Met Arg Arg Ala Leu Pro Ala His Ala Lys Ile
        35                  40                  45
Ser Asp Asp Ala Lys Glu Ala Ile Gln Glu Cys Val Ser Glu Phe Ile
    50                  55                  60
Ser Phe Val Thr Gly Glu Ala Asn Glu Arg Cys Arg Met Gln His Arg
65                  70                  75                  80
Lys Thr Val Asn Ala Glu Asp Ile Val Trp Ala Leu Asn Arg Leu Gly
                85                  90                  95
Phe Asp Asp Tyr Val Val Pro Leu Ser Val Phe Leu His Arg Met Arg
            100                 105                 110
Asp Pro Glu Ala Gly Thr Gly Gly Ala Ala Ala Gly Asp Ser Arg Ala
        115                 120                 125
Val Thr Ser Ala Pro Pro Arg Ala Ala Pro Pro Val Ile His Ala Val
    130                 135                 140
Pro Leu Gln Ala Gln Arg Pro Met Tyr Ala Pro Pro Ala Pro Leu Gln
145                 150                 155                 160
Val Glu Asn Gln Met Gln Arg Pro Val Tyr Ala Pro Pro Ala Pro Val
                165                 170                 175
Gln Val Gln Met Gln Arg Gly Ile Tyr Gly Pro Arg Ala Pro Val His
            180                 185                 190
Gly Tyr Ala Val Gly Met Ala Pro Val Arg Ala Asn Val Gly Gly Gln
        195                 200                 205
Tyr Gln Val Phe Gly Gly Glu Gly Val Met Ala Gln Gln Tyr Tyr Gly
    210                 215                 220
Tyr Gly Tyr Glu Glu Gly Ala Tyr Gly Ala Gly Ser Ser Asn Gly Gly
225                 230                 235                 240
Ala Ala Ile Gly Asp Glu Glu Ser Ser Ser Asn Gly Val Pro Ala Pro
                245                 250                 255
Gly Glu Gly Met Gly Glu Pro Glu Pro Glu Pro Ala Ala Glu Glu Ser
            260                 265                 270
His Asp Lys Pro Val Gln Ser Gly
        275                 280
```

<210> 23
<211> 65
<212> PRT
<213> Artificial Sequence

<220>
<223> LEC1 consensus protein sequence

<221> VARIANT
<222> (1)...(65)
<223> Xaa = Any Amino Acid

<400> 23

```
Arg Glu Gln Asp Xaa Xaa Met Pro Ile Ala Asn Val Ile Arg Ile Met
 1               5                  10                  15
Arg Xaa Xaa Leu Pro Xaa His Ala Lys Ile Ser Asp Asp Ala Lys Glu
            20                  25                  30
Xaa Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Xaa Thr Xaa Glu
        35                  40                  45
Ala Asn Xaa Arg Cys Xaa Xaa Xaa Xaa Arg Lys Thr Xaa Xaa Xaa Glu
    50                  55                  60
Xaa
65
```